

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Martin Roland Jensen  
Soren Mouritsen  
Henrik Elsner  
Iben Dalum



(ii) TITLE OF INVENTION: Modified human TNF-alpha molecules, DNA encoding them, and vaccines containing said modified TNF-alpha or DNA

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Farmaceutisk Laboratorium Ferring A/S  
(B) STREET: Indertoften 10  
(C) CITY: Vanloese  
(E) COUNTRY: Denmark  
(F) POSTAL CODE (ZIP): DK-2720

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/060,294  
(B) FILING DATE: 15-APR-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/044,187  
(B) FILING DATE: 24-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Price, D. Douglas  
(B) REGISTRATION NUMBER: 24,514  
(C) REFERENCE/DOCKET NUMBER: P60953US1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 638-6666  
(B) TELEFAX: (202) 393-5350

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..477

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/codon\_start= 1  
/function= "Antigen"  
/product= "TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/gene= "tnfp2-1"  
/standard\_name= "TNF2-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT CAG TAC ATT AAA GCC AAT 48  
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn  
1 5 10 15

TCT AAA TTC ATC GGT ATA ACT GAG CTG CAG CTC CAG TGG CTG AAC CGC 96  
Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg  
20 25 30

CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG 144  
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln  
35 40 45

CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC 192  
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu  
50 55 60

TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC 240  
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr  
65 70 75 80

ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT 288  
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser  
85 90 95

GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC 336  
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala  
100 105 110

AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG 384  
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu  
115 120 125

AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC 432  
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp  
130 135 140

TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG 477  
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu \*  
145 150 155

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn  
1 5 10 15  
Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg  
20 25 30  
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln  
35 40 45  
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu  
50 55 60  
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr  
65 70 75 80  
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser  
85 90 95  
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala  
100 105 110  
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu  
115 120 125  
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp  
130 135 140  
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu \*  
145 150 155

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..477  
(D) OTHER INFORMATION: /codon\_start= 1

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/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP2-3"
/standard_name= "TNF2-3"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC CAG TAC ATA AAG GCC AAC TCC AAG TTT ATC GGC ATC ACC GAG CTC	240
Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His

1	5	10	15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	20	25	30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	35	40	45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	50	55	60
Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu	65	70	75
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	85	90	95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	100	105	110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	115	120	125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	130	135	140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	145	150	155

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: /codon\_start= 1  
/function= "Antigen"  
/product= "TNF-alpha analog"  
/gene= "tnfp2-4"  
/standard\_name= "TNF2-4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT  
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His



(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
	50					55					60				

Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65					70					75					80	
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
				85					90					95		
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	
			100					105					110			
Lys	Pro	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	
		115					120					125				
Leu	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
	130					135					140					
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..477
  - (D) OTHER INFORMATION: /function= "Antigen"
  - /product= "TNF-alpha analog"
  - /gene= "tnfP2-5"
  - /standard\_name= "TNF2-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	GTC	AGA	TCA	TCT	TCT	CGA	ACC	CCG	AGT	GAC	AAG	CCT	GTA	GCC	CAT	48
Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	
160					165					170					175	
GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	GGG	CAG	CTC	CAG	TGG	CTG	AAC	CGC	96
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	
				180					185					190		
CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	144
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
			195					200					205			
CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	

210	215	220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC			240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr			
225	230	235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT			288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser			
240	245	250	255
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC			336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala			
260	265	270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG			384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu			
275	280	285	
AAG GGT GAC CGA CAG TAC ATT AAG GCC AAT TCG AAG TTC ATT GGC ATC			432
Lys Gly Asp Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile			
290	295	300	
ACT GAG CTG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG			477
Thr Glu Leu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	



115		120		125
Lys Gly Asp Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile				
130		135		140
Thr Glu Leu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *				
145		150		155

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..477
- (D) OTHER INFORMATION:/codon\_start= 1  
/function= "Antigen"  
/product= "TNF-alpha analog"  
/gene= "tnfP2-7"  
/standard\_name= "TNF2-7"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160	165 170 175
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
	180 185 190
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
	195 200 205
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
	210 215 220
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CAG TAC ATC AAA	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Gln Tyr Ile Lys	
	225 230 235
GCT AAC TCC AAA TTC ATC GGC ATC ACC GAA CTG GTT AAC CTC CTC TCT	288
Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Val Asn Leu Leu Ser	
240	245 250 255

GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Gln Tyr Ile Lys	
65 70 75 80	
Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Val Asn Leu Leu Ser	
85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
115 120 125	
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
130 135 140	
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
145 150 155	

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION:1..477  
 (D) OTHER INFORMATION:/codon\_start= 1  
 /function= "Antigen"  
 /product= "TNF-alpha analog"  
 /gene= "tnfp30-1"  
 /standard\_name= "TNF30-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT TTC AAC AAT TTT ACC GTA	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Phe Asn Asn Phe Thr Val	
160 165 170 175	
AGC TTT TGG CTC CGT GTA CCT AAG GTG TCG GCC TCG CAC CTG GAG CGC	96
Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	

290

295

300

TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG  
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu \*  
 305 310 315

477

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Phe Asn Asn Phe Thr Val  
 1 5 10 15  
 Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Arg  
 20 25 30  
 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln  
 35 40 45  
 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu  
 50 55 60  
 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr  
 65 70 75 80  
 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser  
 85 90 95  
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala  
 100 105 110  
 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu  
 115 120 125  
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp  
 130 135 140  
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu \*  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..477

(D) OTHER INFORMATION:/codon\_start= 1  
/function= "Antigen"  
/product= "TNF-alpha analog"  
/gene= "tnfP30-2"  
/standard\_name= "TNF30-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT TTC AAC AAC TTC ACA GTT AGC TTC	144
Arg Ala Asn Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe	
195 200 205	
TGG TTG AGG GTA CCA AAG GTC TCG GCC AGC CAC CTC GAG CAG GTC CTC	192
Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
  1           5           10           15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
          20           25           30
Arg Ala Asn Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe
          35           40           45
Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu
          50           55           60
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
          65           70           75           80
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
          85           90           95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
          100          105          110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
          115          120          125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
          130          135          140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
145          150          155
```

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..477  
(D) OTHER INFORMATION: /codon\_start= 1

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/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP30-3"
/standard_name= "TNF30-3"

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAC AAC TTT ACC GTC TCC TTC TGG CTT CGG GTA CCC AAG GTC AGC	240
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser	
225 230 235	
GCT AGC CAC CTC GAG GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ala Ser His Leu Glu Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His

1	5	10	15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	20	25	30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	35	40	45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	50	55	60
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser	65	70	75
Ala Ser His Leu Glu Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	85	90	95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	100	105	110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	115	120	125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	130	135	140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	145	150	155

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..477
  - (D) OTHER INFORMATION: /function= "Antigen"
  - /product= "TNF-alpha analog"
  - /gene= "tnfp30-4"
  - /standard\_name= "TNF30-4"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	160	165	170	175
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His				



GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA TTT AAT AAT TTC ACC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Phe Asn Asn Phe Thr	
260 265 270	
GTG TCC TTC TGG TTG CGC GTC CCT AAG GTA AGC GCT TCC CAC CTG GAG	384
Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	

Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65					70					75					80	
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
				85					90					95		
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Phe	Asn	Asn	Phe	Thr	
			100					105					110			
Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	
		115					120					125				
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
	130					135					140					
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..477
- (D) OTHER INFORMATION:/codon\_start= 1  
/function= "Antigen"  
/product= "TNF-alpha analog"  
/gene= "tnfp30-5"  
/standard\_name= "TNF30-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG	GTC	AGA	TCA	TCT	TCT	CGA	ACC	CCG	AGT	GAC	AAG	CCT	GTA	GCC	CAT	48
Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	
160					165					170					175	
GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	GGG	CAG	CTC	CAG	TGG	CTG	AAC	CGC	96
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	
			180					185					190			
CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	144
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
			195					200				205				
CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	

210	215	220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC			240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr			
225	230	235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT			288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser			
240	245	250	255
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC			336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala			
	260	265	270
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG			384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu			
	275	280	285
AAG GGT GAC CGA TTC AAC AAT TTC ACC GTA AGC TTC TGG CTT CGC GTC			432
Lys Gly Asp Arg Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val			
	290	295	300
CCT AAG GTG TCT GCG TCG CAC CTC GAA GGG ATC ATT GCC CTC TAG			477
Pro Lys Val Ser Ala Ser His Leu Glu Gly Ile Ile Ala Leu *			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
	50					55					60				
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr
65					70					75					80
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser
			85					90						95	
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala
		100						105					110		
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu

115	120	125
Lys Gly Asp Arg Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val		
130	135	140
Pro Lys Val Ser Ala Ser His Leu Glu Gly Ile Ile Ala Leu *		
145	150	155

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION:1..24
  - (C) IDENTIFICATION METHOD: experimental
  - (D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha"  
/product= "Primer binding to TNF-alpha gene"  
/evidence= EXPERIMENTAL  
/standard\_name= "TNF-alpha Primer I"  
/label= Primer1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GACAAGCCCA TGGTCAGATC ATCT

24

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION:1..30
  - (C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha"  
/product= "Primer binding to TNF-alpha gene"  
/evidence= EXPERIMENTAL  
/standard\_name= "TNF-alpha Primer II"  
/label= Primer2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCTCTAGAGG GCAATGATCC CAAAGTAGAC

30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION:1..21  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha"  
/product= "Primer binding to TNF-alpha gene"  
/evidence= EXPERIMENTAL  
/standard\_name= "TNF-alpha Primer III"  
/label= Primer3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCCAAAGTAG ACCTGCCCAG A

21

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion\_seq
- (B) LOCATION:7..51
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut2-1""  
/label= mut2-1  
/note= "Primer "mut2-1" is a synthetically synthesised  
69-mer oligonucleotide comprising DNA encoding the human  
T cell epitope P2 between stretches of DNA homologous to  
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACCCCGAGTC AGTACATTAA AGCCAATTCT AAATTCATCG GTATAACTGA GCTGCAGCTC	60
CAGTGGCTG	69

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion\_seq
- (B) LOCATION:15..59
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut2-3""  
/label= mut2-3  
/note= "Primer "mut2-3" is a synthetically synthesised  
73-mer oligonucleotide comprising DNA encoding the human  
T cell epitope P2 between stretches of DNA homologous to  
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCCAGGTCCT CTTCCAGTAC ATAAAGGCCA ACTCCAAGTT TATCGGCATC ACCGAGCTCA	60
TCAGCCGCAT CGC	73

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 75 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens  
(ix) FEATURE:  
    (A) NAME/KEY: insertion\_seq  
    (B) LOCATION:12..56  
    (C) IDENTIFICATION METHOD: experimental  
    (D) OTHER INFORMATION:/function= "Primer for PCR cloning  
        of DNA encoding TNF-alpha analog"  
        /evidence= EXPERIMENTAL  
        /organism= "Homo sapiens"  
        /standard\_name= "Primer "mut2-4""  
        /label= mut2-4  
        /note= "Primer "mut2-4" is a synthetically synthesised  
            75-mer oligonucleotide comprising DNA encoding the human  
            T cell epitope P2 between stretches of DNA homologous to  
            stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AGTCGGTCAC CGAGCTCCGT GATGCCGATG AATTTCAAT TGGCCTTGAT ATACTGGGGC	60
TTGGCCTCAG CCCCC	75

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 75 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens  
(ix) FEATURE:  
    (A) NAME/KEY: insertion\_seq  
    (B) LOCATION:8..52  
    (C) IDENTIFICATION METHOD: experimental  
    (D) OTHER INFORMATION:/function= "Primer for PCR cloning  
        of DNA encoding TNF-alpha analog"  
        /evidence= EXPERIMENTAL

/organism= "Homo sapiens"  
/standard\_name= "Primer "mut2-5"  
/label= mut2-5  
/note= "Primer "mut2-5" is a synthetically synthesised  
75-mer oligonucleotide comprising DNA encoding the human  
T cell epitope P2 between stretches of DNA homologous to  
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAAGGGTGAC CGACAGTACA TTAAGGCCAA TTCGAAGTTC ATTGGCATCA CTGAGCTGTC 60  
TGGGCAGGTC TACTT 75

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion\_seq
- (B) LOCATION:14..58
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut2-7"  
/label= mut2-7  
/note= "Primer "mut2-7" is a synthetically synthesised  
80-mer oligonucleotide comprising DNA encoding the human  
T cell epitope P2 between stretches of DNA homologous to  
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CACCCATGTG CTCCAGTACA TCAAAGCTAA CTCCAAATTC ATCGGCATCA CCGAACTGGT 60  
TAACCTCCTC TCTGCCATCA 80

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: insertion\_seq
  - (B) LOCATION:10..72
  - (C) IDENTIFICATION METHOD: experimental
  - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut30-1"  
/label= mut30-1  
/note= "Primer "mut30-1" is a synthetically synthesised 96-mer oligonucleotide comprising DNA encoding the human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACCCCGAGTT TCAACAATTT TACCGTAAGC TTTTGGCTCC GTGTACCTAA GGTGTCGGCC	60
TCGCACCTGG AGCGCCGGGC CAATGCCCTC CTGGCC	96

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: insertion\_seq
  - (B) LOCATION:12..74
  - (C) IDENTIFICATION METHOD: experimental
  - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut30-2"  
/label= mut30-2

/note= "Primer "mut30-2" is a synthetically synthesised 100-mer oligonucleotide comprising DNA encoding human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
TCCTGGCCAA TTTCAACAAC TTCACAGTTA GCTTCTGGTT GAGGGTACCA AAGGTCTCGG      60
CCAGCCACCT CGAGCAGGTC CTCTTCAAGG GCCAAGGCTG                             100
```

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion\_seq
- (B) LOCATION:12..74
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut30-3"  
/label= mut30-3  
/note= "Primer "mut30-3" is a synthetically synthesised 100-mer oligonucleotide comprising DNA encoding human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
CCCAGGTCCT CTTCAACAAC TTTACCGTCT CCTTCTGGCT TCGGGTACCC AAGGTCAGCG      60
CTAGCCACCT CGAGGTCTCC TACCAGACCA AGGTCAACCT                             100
```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: insertion\_seq

(B) LOCATION:15..77

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut30-4"  
/label= mut30-4  
/note= "Primer "mut30-4" is a synthetically synthesised  
100-mer oligonucleotide comprising DNA encoding human T  
cell epitope P30 between stretches of DNA homologous to  
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
AGTCGGTCAC CCTTCTCCAG GTGGGAAGCG CTTACCTTAG GGACGCGCAA CCAGAAGGAC      60
ACGGTGAAAT TATTAAATGG GGTCTCCCTC TGGCAGGGGC                          100
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: insertion\_seq

(B) LOCATION:14..76

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/function= "Primer for PCR cloning  
of DNA encoding TNF-alpha analog"  
/evidence= EXPERIMENTAL  
/organism= "Homo sapiens"  
/standard\_name= "Primer "mut30-5"  
/label= mut30-5  
/note= "Primer "mut30-5" is a synthetically synthesised  
100-mer oligonucleotide comprising DNA encoding human T  
cell epitope P30 between stretches of DNA homologous to  
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GAAGGGTGAC CGATTCAACA ATTTACCGT AAGCTTCTGG CTTGCGTCC CTAAGGTGTC 60  
TGGTTCGCAC CTCGAAGGGA TCATTGCCCT CTAGAGTCGA 100

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..25
- (D) OTHER INFORMATION:/label= Pep2-1  
/note= "Pep2-1 is a synthetically prepared truncated form  
of a TNF-alpha analog comprising the human T cell epitope  
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly  
1 5 10 15  
Ile Thr Glu Leu Gln Leu Gln Trp Leu  
20 25

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..25
- (D) OTHER INFORMATION:/label= Pep2-3  
/note= "Pep2-3 is a synthetically prepared truncated form  
of a TNF-alpha analog comprising the human T cell epitope  
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Ser Gln Val Leu Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly  
1                      5                      10                      15  
Ile Thr Glu Leu Ile Ser Arg Ile Ala  
                    20                      25

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION:1..25
  - (D) OTHER INFORMATION:/label= Pep2-4  
/note= "Pep2-4 is a synthetically prepared truncated form  
of a TNF-alpha analog comprising the human T cell epitope  
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Ala Glu Ala Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly  
1                      5                      10                      15  
Ile Thr Glu Leu Gly Asp Arg Leu Ser  
                    20                      25

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..25

(D) OTHER INFORMATION:/label= Pep2-5

/note= "Pep2-5 is a synthetically prepared truncated form  
of a TNF-alpha analog comprising the human T cell epitope  
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Glu	Lys	Gly	Asp	Arg	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly
1				5					10					15	
Ile	Thr	Glu	Leu	Ser	Gly	Gln	Val	Tyr							
			20					25							

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..31

(D) OTHER INFORMATION:/label= Pep30-1

/note= "Pep30-1 is a synthetically prepared truncated  
form of a TNF-alpha analog comprising human T cell  
epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ser	Arg	Thr	Pro	Ser	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5					10					15	
Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Arg	Arg	Ala	Asn	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..31

(D) OTHER INFORMATION:/label= Pep30-2

/note= "Pep30-2 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg  
1 5 10 15

Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu Phe Lys  
20 25 30

B<sup>1</sup>  
(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..31

(D) OTHER INFORMATION:/label= Pep30-3

/note= "Pep30-3 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Tyr Ser Gln Val Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg  
1 5 10 15

Val Pro Lys Val Ser Ala Ser His Leu Glu Val Ser Tyr Gln Thr  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION:1..31
  - (D) OTHER INFORMATION:/label= Pep30-4  
 /note= "Pep30-4 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Gln Arg Glu Thr Pro Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg  
 1 5 10 15  
 Val Pro Lys Val Ser Ala Ser His Leu Glu Lys Gly Asp Arg Leu  
 20 25 30

B' (2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION:1..31
  - (D) OTHER INFORMATION:/label= Pep30-5  
 /note= "Pep30-5 is a synthetically prepared truncated



form of a TNF-alpha analog comprising the human T cell  
epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

B<sup>1</sup>

Glu	Lys	Gly	Asp	Arg	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5					10					15	
Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gly	Ile	Ile	Ala	Leu	
			20					25					30		

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